

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/785,607A
Source: IFW/6
Date Processed by STIC: 7/15/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

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- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/785,607A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleic
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4 Non-ASCII The submitted file was **not saved** in ASCII(DOS) text, as required by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 Skipped Sequences
(NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11 Use of <220>
→ Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/785,607A

DATE: 07/15/2005

TIME: 11:09:25

Input Set : A:\39780-1216R1C1D5 SAVED JULY 7 2005.TXT
 Output Set: N:\CRF4\07152005\J785607A.raw

4 <110> APPLICANT: Ashkenazi, Avi J.
 5 Fong, Sherman
 6 Goddard, Audrey
 7 Gurney, Austin L.
 8 Napier, Mary A.
 9 Tumas, Daniel
 10 Wood, William I.
 12 <120> TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR
 13 THE TREATMENT OF DISEASES CHARACTERIZED BY A-33 RELATED
 14 ANTIGENS
 16 <130> FILE REFERENCE: 39780-1216R1C1D5
 18 <140> CURRENT APPLICATION NUMBER: US 10/785,607A
 19 <141> CURRENT FILING DATE: 2004-02-24
 21 <150> PRIOR APPLICATION NUMBER: US 09/953,499
 22 <151> PRIOR FILING DATE: 2001-09-14
 24 <150> PRIOR APPLICATION NUMBER: US 09/254,465
 25 <151> PRIOR FILING DATE: 1999-03-05
 27 <150> PRIOR APPLICATION NUMBER: PCT/US98/24855
 28 <151> PRIOR FILING DATE: 1998-11-20
 30 <150> PRIOR APPLICATION NUMBER: PCT/US98/19437
 31 <151> PRIOR FILING DATE: 1998-09-17
 33 <160> NUMBER OF SEQ ID NOS: 30
 35 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 37 <210> SEQ ID NO: 1
 38 <211> LENGTH: 299
 39 <212> TYPE: PRT
 40 <213> ORGANISM: Homo sapiens
 42 <400> SEQUENCE: 1
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 44 1 5 10 15
 45 Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
 46 20 25 30
 47 Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
 48 35 40 45
 49 Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
 50 50 55 60
 51 Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
 52 65 70 75 80
 53 Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
 54 85 90 95
 55 Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
 56 100 105 110
 57 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val

*Does Not Comply
 :corrected Diskette Neede*

pp 3-4

RAW SEQUENCE LISTING DATE: 07/15/2005
 PATENT APPLICATION: US/10/785,607A TIME: 11:09:25

Input Set : A:\39780-1216R1C1D5 SAVED JULY 7 2005.TXT
 Output Set: N:\CRF4\07152005\J785607A.raw

58 115 120 125
 59 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
 60 130 135 140
 61 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
 62 145 150 155 160
 63 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
 64 165 170 175
 65 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
 66 180 185 190
 67 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
 68 195 200 205
 69 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
 70 210 215 220
 71 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
 72 225 230 235 240
 73 Ala Ala Val Leu Val Thr Leu Ile Leu Gly Ile Leu Val Phe Gly
 74 245 250 255
 75 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
 76 260 265 270
 77 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
 78 275 280 285
 79 Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
 80 290 295
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 84 <211> LENGTH: 321
 85 <212> TYPE: PRT
 86 <213> ORGANISM: Homo sapiens
 88 <400> SEQUENCE: 2
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 91 Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr Gly Pro
 92 20 25 30
 93 Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro Leu Gln Gly
 94 35 40 45
 95 Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg Gly Ser Asp Pro
 96 50 55 60
 97 Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp His Ile Gln Gln Ala
 98 65 70 75 80
 99 Lys Tyr Gln Gly Arg Leu His Val Ser His Lys Val Pro Gly Asp Val
 100 85 90 95
 101 Ser Leu Gln Leu Ser Thr Leu Glu Met Asp Asp Arg Ser His Tyr Thr
 102 100 105 110
 103 Cys Glu Val Thr Trp Gln Thr Pro Asp Gly Asn Gln Val Val Arg Asp
 104 115 120 125
 105 Lys Ile Thr Glu Leu Arg Val Gln Lys Leu Ser Val Ser Lys Pro Thr
 106 130 135 140
 107 Val Thr Thr Gly Ser Gly Tyr Gly Phe Thr Val Pro Gln Gly Met Arg
 108 145 150 155 160
 109 Ile Ser Leu Gln Cys Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile

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Input Set : A:\39780-1216R1C1D5 SAVED JULY 7 2005.TXT
Output Set: N:\CRF4\07152005\J785607A.raw

110 165 170 175
111 Trp Tyr Lys Gln Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr
112 180 185 190
113 Leu Ser Thr Leu Leu Phe Lys Pro Ala Val Ile Ala Asp Ser Gly Ser
114 195 200 205
115 Tyr Phe Cys Thr Ala Lys Gly Gln Val Gly Ser Glu Gln His Ser Asp
116 210 215 220
117 Ile Val Lys Phe Val Val Lys Asp Ser Ser Lys Leu Leu Lys Thr Lys
118 225 230 235 240
119 Thr Glu Ala Pro Thr Thr Met Thr Tyr Pro Leu Lys Ala Thr Ser Thr
120 245 250 255
121 Val Lys Gln Ser Trp Asp Trp Thr Thr Asp Met Asp Gly Tyr Leu Gly
122 260 265 270
123 Glu Thr Ser Ala Gly Pro Gly Lys Ser Leu Pro Val Phe Ala Ile Ile
124 275 280 285
125 Leu Ile Ile Ser Leu Cys Cys Met Val Val Phe Thr Met Ala Tyr Ile
126 290 295 300
127 Met Leu Cys Arg Lys Thr Ser Gln Gln Glu His Val Tyr Glu Ala Ala
128 305 310 315 320
129 Arg

133 <210> SEQ ID NO: 3

134 <211> LENGTH: 390

135 <212> TYPE: DNA

136 <213> ORGANISM: Artificial Sequence

138 <220> FEATURE:

139 <223> OTHER INFORMATION: Artificial sequence

141 <400> SEQUENCE: 3

142 cttcttgcca actggtatca ccttcaagtc cgtgacacgg gaagacactg ggacatacac 60
143 ttgtatggtc tctgaggaag gcccacacag ctatggggag gtcaagggtca agtcatcg 120
144 gcttgcct ccatccaagc ctacagttaa catcccccc tctgccccca ttggaaaccg 180
145 ggcagtgtcg acatgctcag aacaagatgg ttcccccacct tctgaataca cctggttcaa 240
146 agatggata gtgatgccta cgaatccaa aagcaccgt gccttcagca actttccta 300
147 tgtcctgaat cccacaacag gagagctggt ctttgcata cttgtcagcc ctgataactgg 360
148 agaatacagc tgtgaggcac ggaatgggta 390

150 <210> SEQ ID NO: 4

151 <211> LENGTH: 726

152 <212> TYPE: DNA

153 <213> ORGANISM: Artificial Sequence

155 <220> FEATURE:

156 <223> OTHER INFORMATION: Artificial sequence

158 <400> SEQUENCE: 4

159 tctcagtccc ctgcgtgtag tcgcggagct gtgttctgtt tcccaggagt cttcggcgg 60
160 ctgttgtgtc cagggtgcgc tgatcgcgtt ggggacaaag gcgcaagtc gagaggaaac 120
161 ttttgtgcct cttcatattt ggcgttccgt tttgtgtccct ggcattggc agtgttacag 180
162 ttgcactctt ctgaacctga agtcagaatt cctgagaata atcctgtgaa gttgtccctgt 240
163 gcctactcgg gctttcttc tccccgtgtt gagttggaaat ttgaccaagg agacaccacc 300
164 agactcggtt gctataataa caagatcaca gcttcctatg aggaccgggt gaccttctt 360
165 ccaactggta tcaccccaa gtccgtgaca cggaaagaca ctgggacata cacttgtatg 420
166 gtctctgagg aaggccgcaa cagctatggg gaggtcaagg tcaagctcat cgtgcttgc 480

Insufficient explanation - give source of genetic material (see item 11 on Error Summary sheet)

RAW SEQUENCE LISTING

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Input Set : A:\39780-1216R1C1D5 SAVED JULY 7 2005.TXT
 Output Set: N:\CRF4\07152005\J785607A.raw

167 cctccatcca agcctacagt taacatcccc tcctctgccca ccattggaa ccgggcagtg 540
 168 ctgacatgt cagaacaaga tggttcccca ccttctgaat acacctgtt caaagatggg 600
 169 atagtgtgc ctacgaatcc caaaaagcacc cgtgccttca gcaactctc ctatgtcctg 660
 170 aatccccacaa caggagagct ggtcttgat cccctgttag cctctgatac tggagaatac 720
 171 agctgt 726
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 174 <211> LENGTH: 1503
 175 <212> TYPE: DNA
 176 <213> ORGANISM: Artificial Sequence
 178 <220> FEATURE:
 179 <223> OTHER INFORMATION: Artificial sequence
 181 <400> SEQUENCE: 5

182 gcaggcaaag taccagggcc gcctgcatgt gagccacaag gttccaggag atgtatccct 60
 183 ccaattgagc accctggaga tggatgaccg gagccactac acgtgtgaag tcacctggca 120
 184 gactcctgat ggcaaccaag tcgtgagaga taagattact gagctccgtg tccagaaact 180
 185 ctctgtctcc aagcccacag tgacaactgg cagcggttat ggcttcacgg tgccccaggg 240
 186 aatgaggatt agcctcaat gccagggttc ggggttctcc tcccatcaat tatatttgg 300
 187 ataagcaaca gactaataac cagggAACCC atcaaagttag caaccctaag taccttactc 360
 188 ttcaagcctg cggtgatagc cgactcaggc tcctatttct gcactgccaa gggccagggtt 420
 189 ggctctgagc agcacagcga cattgtgaag tttgtggta aagactcctc aaagctactc 480
 190 aagaccaaga ctgaggcacc tacaaccatg acataaccct tgaaagcaac atctacagt 540
 191 aacgactcct gggactggac cactgacatg gatggctacc ttggagagac cagtgctgg 600
 192 ccagggaaaga gcctgcctgt ctttgcattc atcctcatca ttccttggc 660
 193 gtttttacca tggcctatata catgctctgt cggaagacat cccaaacaaga gcatgtctac 720
 194 gaagcagcca gggcacatgc cagagaggcc aacgactctg gagaaccat gaggggtggcc 780
 195 atcttcgcaa gtggctgctc cagtgtatgg ccaacttccc agaatctgg gcaacaacta 840
 196 ctctgatgag ccctgcatag gacaggagta ccagatcatc gcccagatca atggcaacta 900
 197 cgcccgccctg ctggacacag ttctctggta ttatgagtt ctggccactg agggcaaaag 960
 198 tgtctgttaa aaatgccccca tttagggcagg atctgctgac ataattgcct agtcagtcct 1020
 199 tgccttctgc atggccttct tccctgtac ctctcttccct ggatagccca aagtgtccgc 1080
 200 ctaccaacac tggagccgct gggagtcact ggcttgcct tggaaatttgc cagatgcattc 1140
 201 tcaagtaagc cagctgctgg atttggctct gggcccttct agtatctctg ccgggggctt 1200
 202 ctggtaactcc tctctaaata ccagaggaa gatgcccata gcactaggac ttgttcatca 1260
 203 tgcctacaga cactattcaa ctttggcatc ttgccaccag aagaccggag gggaggctca 1320
 204 gctctgcccag ctcagaggac cagctataatc caggatcatt tctcttctt cagggccaga 1380
 205 cagttttaa ttgaaattgt tatttcacag gccagggttc agttctgctc ctccactata 1440
 206 agtctaattgt tctgactctc tcctggtgct caataatata ctaatcataa cagcaaaaaaa 1500
 207 aaa 1503
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 210 <211> LENGTH: 319
 211 <212> TYPE: PRT
 212 <213> ORGANISM: Homo sapiens
 214 <400> SEQUENCE: 6

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 216 1 5 10 15
 217 Val Thr Val Asp Ala Ile Ser Val Glu Thr Pro Gln Asp Val Leu Arg
 218 20 25 30
 219 Ala Ser Gln Gly Lys Ser Val Thr Leu Pro Cys Thr Tyr His Thr Ser
 220 35 40 45

*This error appears in
 subsequent sequences, too.*

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/785,607A

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Input Set : A:\39780-1216R1C1D5 SAVED JULY 7 2005.TXT
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221 Thr Ser Ser Arg Glu Gly Leu Ile Gln Trp Asp Lys Leu Leu Leu Thr
222 50 55 60
223 His Thr Glu Arg Val Val Ile Trp Pro Phe Ser Asn Lys Asn Tyr Ile
224 65 70 75 80
225 His Gly Glu Leu Tyr Lys Asn Arg Val Ser Ile Ser Asn Asn Ala Glu
226 85 90 95
227 Gln Ser Asp Ala Ser Ile Thr Ile Asp Gln Leu Thr Met Ala Asp Asn
228 100 105 110
229 Gly Thr Tyr Glu Cys Ser Val Ser Leu Met Ser Asp Leu Glu Gly Asn
230 115 120 125
231 Thr Lys Ser Arg Val Arg Leu Leu Val Leu Val Pro Pro Ser Lys Pro
232 130 135 140
233 Glu Cys Gly Ile Glu Gly Glu Thr Ile Ile Gly Asn Asn Ile Gln Leu
234 145 150 155 160
235 Thr Cys Gln Ser Lys Glu Gly Ser Pro Thr Pro Gln Tyr Ser Trp Lys
236 165 170 175
237 Arg Tyr Asn Ile Leu Asn Gln Glu Gln Pro Leu Ala Gln Pro Ala Ser
238 180 185 190
239 Gly Gln Pro Val Ser Leu Lys Asn Ile Ser Thr Asp Thr Ser Gly Tyr
240 195 200 205
241 Tyr Ile Cys Thr Ser Ser Asn Glu Glu Gly Thr Gln Phe Cys Asn Ile
242 210 215 220
243 Thr Val Ala Val Arg Ser Pro Ser Met Asn Val Ala Leu Tyr Val Gly
244 225 230 235 240
245 Ile Ala Val Gly Val Val Ala Ala Leu Ile Ile Ile Gly Ile Ile Ile
246 245 250 255
247 Tyr Cys Cys Cys Cys Arg Gly Lys Asp Asp Asn Thr Glu Asp Lys Glu
248 260 265 270
249 Asp Ala Arg Pro Asn Arg Glu Ala Tyr Glu Glu Pro Pro Glu Gln Leu
250 275 280 285
251 Arg Glu Leu Ser Arg Glu Arg Glu Glu Glu Asp Asp Tyr Arg Gln Glu
252 290 295 300
253 Glu Gln Arg Ser Thr Gly Arg Glu Ser Pro Asp His Leu Asp Gln
254 305 310 315
257 <210> SEQ ID NO: 7
258 <211> LENGTH: 2181
259 <212> TYPE: DNA
260 <213> ORGANISM: Homo sapiens
262 <400> SEQUENCE: 7
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264 tttgagcctc tttggtagca ggaggctgga agaaaggaca gaagtagctc tggctgtat 120
265 ggggatctta ctgggcctgc tactcctggg gcacctaaca gtggacactt atggccgtcc 180
266 catcctggaa gtgccagaga gtgtAACAGG accttggaaa ggggatgtga atcttccctg 240
267 cacctatgac cccctgcaag gctacaccca agtcttggtg aagtggotgg tacaacgtgg 300
268 ctcagaccct gtcaccatct ttctacgtga ctcttctgga gaccatatcc agcaggcaaa 360
269 gtaccagggc cgcctgcatg tgagccacaa ggttccagga gatgtatccc tccaaattgag 420
270 caccctggag atggatgacc ggagccacta cacgtgtgaa gtcacctggc agactcctga 480
271 tggcaaccaa gtcgtgagag ataagattac tgagctccgt gtccagaaac tctctgtctc 540
272 caagcccaca gtgacaactg gcagcggtt tggcttcacg gtgccccagg gaatgaggat 600

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/785,607A

DATE: 07/15/2005

TIME: 11:09:26

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